



SEQUENCE LISTING

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MORIMOTO, IKUO
MIYAMURA, KOICHI

<120> CELL SEPARATION DEVICE AND SEPARATION METHOD

<130> ASAHI-1-PC-1

<140> 09/701,001

<141> 2000-11-22

<150> PCT/JP99/02711

<151> 1999-05-24

<150> JP 159957

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<150> JP 163023

<151> 1998-05-26

<160> 66

<170> PatentIn Ver. 2.1

<210> 1

<211> 5

<212> PRT

<213> Mus sp.

<400> 1

Asp Tyr Val Ile Asn
1 5

*see EP 0365,205
Figs 2 and 3
= CDR1 of anti Lew 3a*

<210> 2

<211> 17

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<213> Mus sp.

<400> 2

Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe Lys
1 5 10 15

Gly

= CDR2 of anti Lew 3a

<210> 3

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<212> PRT

<213> Mus sp.

<400> 3

Arg Gly Thr Gly Thr Gly Phe Ala Tyr
1 5

= CDR3 of anti Lew 3a

Handwritten: H chain CDR1

Handwritten: H chain CDR2

Handwritten: H chain CDR3

L chain
CDR 1
 <210> 4
 <211> 15
 <212> PRT
 <213> Mus sp.

<400> 4 / / / / / / / / / / / / / / / /
 Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
 1 5 10 15

CDR 1 of anti-LawBa

L chain
CDR 2
 <210> 5
 <211> 7
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<400> 5
 Ala Ala Ser Asn Leu Glu Ser
 1 5

CDR 2 of anti-LawBa

L chain
CDR 3
 <210> 6
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<400> 6
 Gln Gln Ser Ser Glu Asp Pro Pro Thr
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CDR 3 of anti-LawBa

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 Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala
 1 5 10 15
 tct gga tac aca ttc act gac tat gtt ata aac tgg ttg aac cag aga 96
 Ser Gly Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg
 20 25 30
 act gga cag ggc ctt gag tgg att gga gag att tat cct gga agt ggt 144
 Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly
 35 40 45
 agt gct tac tac aat gag atg ttc aag ggc aag gcc aca ctg act gca 192
 Ser Ala Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala
 50 55 60

gac aaa tcc tcc aac aca gcc tac atg cag ctc agc agc ctg aca tct 240
 Asp Lys Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
 65 70 75 80

gag gac tct gcg gtc tat ttc tgt gca aga cgc gga act ggg acg ggg 288
 Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly
 85 90 95

ttt gct tac tgg ggc cga ggg act ctg gtc act gtc tct gca 330
 Phe Ala Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ala
 100 105 110

<210> 8

<211> 309

<212> DNA

<213> Mus sp.

<220>

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<222> (1) .. (309)

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 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 1 5 10 15

gcc agc caa agt gtt gat tat gat ggt gat agt tat atg aac tgg tac 96
 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr
 20 25 30

caa cag aaa cca gga cag cca ccc aaa ctc ctc atc tat gct gca tcc 144
 Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser
 35 40 45

aat cta gaa tct ggg atc cca gcc agg ttt agt ggc agt ggg tct ggg 192
 Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 50 55 60

aca gac ttc acc ctc aac atc cat cct gtg gag gag gag gat gct gca 240
 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala
 65 70 75 80

acc tat tac tgt cag caa agt agt gag gat cct ccg acg ttc ggt gga 288
 Thr Tyr Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly
 85 90 95

ggc acc aag ctg gaa atc aaa 309
 Gly Thr Lys Leu Glu Ile Lys
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<210> 9

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<212> DNA

<213> Mus sp.

<220>
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single chain Ab to CD4

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Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala	
1				5					10					15		
gcc	cag	ccg	gcc	atg	gcc	gac	att	gtg	ctg	acc	caa	tct	cca	gct	tct	96
Ala	Gln	Pro	Ala	Met	Ala	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	
		20						25					30			
ttg	gct	gtg	tct	cta	ggg	cag	agg	gcc	acc	atc	tcc	tgc	aag	gcc	agc	144
Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	
		35					40					45				
caa	agt	gtt	gat	tat	gat	ggg	gat	agt	tat	atg	aac	tgg	tac	caa	cag	192
Gln	Ser	Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	
	50					55					60					
aaa	cca	gga	cag	cca	ccc	aaa	ctc	ctc	atc	tat	gct	gca	tcc	aat	cta	240
Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	
65					70				75					80		
gaa	tct	ggg	atc	cca	gcc	agg	ttt	agt	ggc	agt	ggg	tct	ggg	aca	gac	288
Glu	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	
				85				90						95		
ttc	acc	ctc	aac	atc	cat	cct	gtg	gag	gag	gag	gat	gct	gca	acc	tat	336
Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	
		100						105						110		
tac	tgt	cag	caa	agt	agt	gag	gat	cct	ccg	acg	ttc	ggg	gga	ggc	acc	384
Tyr	Cys	Gln	Gln	Ser	Ser	Glu	Asp	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	
		115				120						125				
aag	ctg	gaa	atc	aaa	ggg	gga	ggc	ggg	tca	ggc	gga	ggg	ggc	tcc	gga	432
Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
130					135			140								
ggg	ggc	gga	tgc	cag	gtt	cag	ctg	cag	cag	tct	gga	cct	gag	ctg	gtg	480
Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	
145				150				155						160		
aag	cct	ggg	gct	tca	gtg	aag	atg	tcc	tgc	aag	gct	tct	gga	tac	aca	528
Lys	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	
				165				170						175		
ttc	act	gac	tat	gtt	ata	aac	tgg	ttg	aac	cag	aga	act	gga	cag	ggc	576
Phe	Thr	Asp	Tyr	Val	Ile	Asn	Trp	Leu	Asn	Gln	Arg	Thr	Gly	Gln	Gly	
		180				185						190				
ctt	gag	tgg	att	gga	gag	att	tat	cct	gga	agt	ggg	agt	gct	tac	tac	624
Leu	Glu	Trp	Ile	Gly	Glu	Ile	Tyr	Pro	Gly	Ser	Gly	Ser	Ala	Tyr	Tyr	
	195				200			205								

CD R 2

aat gag atg ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc 672
 Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
 210 215 220

aac aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg 720
 Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala
 225 230 235 240

gtc tat ttc tgt gca aga cgc gga act ggg acg ggg ttt gct tac tgg 768
 Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp
 245 250 255

ggc cga ggg act ctg gtc act gtc tct gca gcg gcc gca gac tac aag 816
 Gly Arg Gly Thr Leu Val Thr Val Ser Ala Ala Ala Asp Tyr Lys
 260 265 270

gat gac gat gac aaa ggc tcg agc gag cag aag ctg atc agc gaa gag 864
 Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
 275 280 285

gat ctg ggc tcg agg tcg acc cac cat cat cat cac cac ggg tcg acc 912
 Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr
 290 295 300

aaa tgataagctt 925
 Lys
 305

<210> 10
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<220>
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 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

gcc cag ccg gcc atg gcc cag gtt cag ctg cag cag tct gga cct gag 96
 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu
 20 25 30

ctg gtg aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 144
 Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
 35 40 45

tac aca ttc act gac tat gtt ata aac tgg ttg aac cag aga act gga 192
 Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly
 50 55 60

cag ggc ctt gag tgg att gga gag att tat cct gga agt ggt agt gct 240
 Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala
 65 70 75 80

tac	tac	aat	gag	atg	ttc	aag	ggc	aag	gcc	aca	ctg	act	gca	gac	aaa	288
Tyr	Tyr	Asn	Glu	Met	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	
				85					90						95	
tcc	tcc	aac	aca	gcc	tac	atg	cag	ctc	agc	agc	ctg	aca	tct	gag	gac	336
Ser	Ser	Asn	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	
			100					105					110			
tct	gcg	gtc	tat	ttc	tgt	gca	aga	cgc	gga	act	ggg	acg	ggg	ttt	gct	384
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Arg	Gly	Thr	Gly	Thr	Gly	Phe	Ala	
		115					120					125				
tac	tgg	ggc	cga	ggg	act	ctg	gtc	act	gtc	tct	gca	ggg	gga	ggc	ggg	432
Tyr	Trp	Gly	Arg	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	
	130					135					140					
tca	ggc	gga	ggt	ggc	tcc	gga	ggt	ggc	gga	tcg	gac	att	gtg	ctg	acc	480
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Leu	Thr	
	145				150					155					160	
caa	tct	cca	gct	tct	ttg	gct	gtg	tct	cta	ggg	cag	agg	gcc	acc	atc	528
Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	
				165					170					175		
tcc	tgc	aag	gcc	agc	caa	agt	gtt	gat	tat	gat	ggg	gat	agt	tat	atg	576
Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	
			180					185					190			
aac	tgg	tac	caa	cag	aaa	cca	gga	cag	cca	ccc	aaa	ctc	ctc	atc	tat	624
Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	
		195					200					205				
gct	gca	tcc	aat	cta	gaa	tct	ggg	atc	cca	gcc	agg	ttt	agt	ggc	agt	672
Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	
	210					215					220					
ggg	tct	ggg	aca	gac	ttc	acc	ctc	aac	atc	cat	cct	gtg	gag	gag	gag	720
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Glu	
	225				230				235						240	
gat	gct	gca	acc	tat	tac	tgt	cag	caa	agt	agt	gag	gat	cct	ccg	acg	768
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser	Glu	Asp	Pro	Pro	Thr	
				245					250					255		
ttc	ggg	gga	ggc	acc	aag	ctg	gaa	atc	aaa	gcg	gcc	gca	gac	tac	aag	816
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Ala	Ala	Ala	Asp	Tyr	Lys	
			260					265					270			
gat	gac	gat	gac	aaa	ggc	tcg	agc	gag	cag	aag	ctg	atc	agc	gaa	gag	864
Asp	Asp	Asp	Asp	Lys	Gly	Ser	Ser	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	
			275				280					285				
gat	ctg	ggc	tcg	agg	tcg	acc	cac	cat	cat	cat	cac	cac	ggg	tcg	acc	912
Asp	Leu	Gly	Ser	Arg	Ser	Thr	His	His	His	His	His	His	Gly	Ser	Thr	
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aaa tgataagctt
Lys
305

925

<210> 11
<211> 28
<212> DNA
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<220>
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DNA primer for PCR

<400> 11
aagcttatga accggggagt ccctttta

28

<210> 12
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 12
gcggccgctc acttgatc gtcgtccttg tagtctggct gcaccggggt ggacca

56

<210> 13
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 13
gggaattcat graatgsasc tgggtywtgc tctt

34

<210> 14
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<212> DNA
<213> Artificial Sequence

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DNA primer for PCR

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DNA primer for PCR

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<223> a, t, c, g, other or unknown
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<223> a, t, c, g, other or unknown
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29

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<220>
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DNA primer for PCR

28

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<210> 17
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<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

33

<210> 18
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Single strand
 DNA primer for PCR

<400> 18
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<210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Single strand
 DNA primer for PCR

<400> 19
 caggatccgc tgcagcagtc tggacct 27

<210> 20
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Single strand
 DNA primer for PCR

<400> 20
 tgggcccgc gttttggctg cagagac 27

<210> 21
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Single strand
 DNA primer for PCR

<400> 21
 tcatgaaata cctgctgccg accgctgctg ctggctctgct gctcctcgcg gccag 56

<210> 22
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 22

tgcggccgca gccatggtgt ttgcggccat cgccggctgg gccgcgagga gcagca 56

<210> 23

<211> 56

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Single strand
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<400> 23

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<210> 24

<211> 57

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Single strand
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<210> 25

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 25

tgcggccgca gactacaagg atg 23

<210> 26

<211> 56

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 26

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<210> 27
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Single strand
 DNA primer for PCR

<400> 27
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<210> 28
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 <223> Description of Artificial Sequence: Single strand
 DNA primer for PCR

<400> 28
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 DNA primer for PCR

<400> 29
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<210> 30
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 DNA primer for PCR

<400> 30
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<210> 31
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 <212> DNA
 <213> Artificial Sequence

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<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 31

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35

<210> 32

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

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56

<210> 33

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Single strand
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43

<210> 34

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 34

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33

<210> 35

<211> 118

<212> PRT

<213> Mus sp.

<400> 35

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp Gly Arg Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ala
 115

<210> 36
 <211> 111
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 <213> Mus sp.

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 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30
 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80
 Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser
 85 90 95
 Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

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<220>
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 1 5 10 15

tca gtg aag atg tcc tgc aag gct tct gga tac aca ttc act gac tat 96
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

gtt ata aac tgg ttg aac cag aga act gga cag ggc ctt gag tgg att 144
 Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile
 35 40 45

gga gag att tat cct gga agt ggt agt gct tac tac aat gag atg ttc 192
 Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe
 50 55 60

aag ggc aag gcc aca ctg act gca gac aaa tcc tcc aac aca gcc tac 240
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
 65 70 75 80

atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc tat ttc tgt 288
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

gca aga cgc gga act ggg acg ggg ttt gct tac tgg ggc cga ggg act 336
 Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp Gly Arg Gly Thr
 100 105 110

ctg gtc act gtc tct gca 354
 Leu Val Thr Val Ser Ala
 115

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<220>
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 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

cag agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat 96
 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

ggt gat agt tat atg aac tgg tac caa cag aaa cca gga cag cca ccc 144
 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

aaa	ctc	ctc	atc	tat	gct	gca	tcc	aat	cta	gaa	tct	ggg	atc	cca	gcc	192
Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ala	
	50					55					60					
agg	ttt	agt	ggc	agt	ggg	tct	ggg	aca	gac	ttc	acc	ctc	aac	atc	cat	240
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	
	65				70					75					80	
cct	gtg	gag	gag	gag	gat	gct	gca	acc	tat	tac	tgt	cag	caa	agt	agt	288
Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser	
				85					90					95		
gag	gat	cct	ccg	acg	ttc	ggg	gga	ggc	acc	aag	ctg	gaa	atc	aaa		333
Glu	Asp	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
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Gln	Val	Gln	Leu	Lys	Gln	Ser	Gly	Pro	Gly	Leu	Val	Gln	Pro	Ser	Gln	
	1			5					10					15		
agc	ctg	tcc	ttc	atc	tgc	aca	gtc	tct	ggg	ttc	tca	tta	act	agt	cat	96
Ser	Leu	Ser	Phe	Ile	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Thr	Ser	His	
			20					25					30			
ggg	gta	cac	tgg	gtt	cgc	cag	tct	cca	gga	aag	ggg	ctg	gag	tgg	ctg	144
Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	
		35				40						45				
gga	gtg	ata	tgg	ggg	gct	gga	agg	aca	gac	tat	aat	gca	gct	ttc	ata	192
Gly	Val	Ile	Trp	Gly	Ala	Gly	Arg	Thr	Asp	Tyr	Asn	Ala	Ala	Phe	Ile	
	50					55					60					
tcc	aga	ctg	agc	atc	agc	agg	gac	att	tcc	aag	agc	caa	gtt	ttc	ttt	240
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<220>
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 <222> (1) .. (339)

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gat cag gcc tcc atc tct tgc aga tct agt cag aac ctt gta cac agt 96
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser
 20 25 30

aat gga aat acc tat tta cat tgg tac ctg cag aag cca ggc cag tct 144
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

cca aat ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca 192
 Pro Asn Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60

gac agg ttc agt ggc agt gga tca ggg aca gaa ttc aca ctc aag atc 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile
 65 70 75 80

agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt 288
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95

aca cat gtt ccg ctc acg ttc ggt gct ggg acc aag gtg gag ctg aaa 336
 Thr His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys
 100 105 110

cgg 339
 Arg

<210> 41
 <211> 909
 <212> DNA
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<220>
 <221> CDS
 <222> (1) .. (906)

<400> 41
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 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
 1 5 10 15

aac	gtg	aaa	aaa	tta	tta	ttc	gca	att	cct	tta	gtt	gtt	cct	ttc	tat	96
Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro	Phe	Tyr	
			20					25					30			
gcg	gcc	cag	ccg	gcc	atg	gcc	cag	gtg	aag	ctg	cag	cag	tct	gga	cct	144
Ala	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Gln	Ser	Gly	Pro	
		35					40					45				
ggc	cta	gtg	cag	ccc	tca	cag	agc	ctg	tcc	ttc	atc	tgc	aca	gtc	tct	192
Gly	Leu	Val	Gln	Pro	Ser	Gln	Ser	Leu	Ser	Phe	Ile	Cys	Thr	Val	Ser	
	50					55					60					
ggg	ttc	tca	tta	act	agt	cat	ggg	gta	cac	tgg	gtt	cgc	cag	tct	cca	240
Gly	Phe	Ser	Leu	Thr	Ser	His	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	
	65				70					75					80	
gga	aag	ggg	ctg	gag	tgg	ctg	gga	gtg	ata	tgg	ggg	gct	gga	agg	aca	288
Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Gly	Ala	Gly	Arg	Thr	
			85					90						95		
gac	tat	aat	gca	gct	ttc	ata	tcc	aga	ctg	agc	atc	agc	agg	gac	att	336
Asp	Tyr	Asn	Ala	Ala	Phe	Ile	Ser	Arg	Leu	Ser	Ile	Ser	Arg	Asp	Ile	
			100					105					110			
tcc	aag	agc	caa	gtt	ttc	ttt	aag	atg	aac	agt	ctg	caa	gtt	gat	gac	384
Ser	Lys	Ser	Gln	Val	Phe	Phe	Lys	Met	Asn	Ser	Leu	Gln	Val	Asp	Asp	
		115					120					125				
aca	gcc	ata	tat	tac	tgt	gcc	aga	aat	agg	tac	gag	agc	tac	ttt	gac	432
Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Tyr	Glu	Ser	Tyr	Phe	Asp	
	130					135					140					
tac	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca	ggg	gga	ggc	ggg	480
Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	
	145				150					155					160	
tca	ggc	gga	ggg	ggc	tct	ggc	ggg	ggc	gga	tgc	gac	atc	gag	ctc	act	528
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Glu	Leu	Thr	
			165					170						175		
cag	tct	cca	ctc	tcc	ctg	cct	gtc	agt	ctt	gga	gat	cag	gcc	tcc	atc	576
Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	
			180					185					190			
tct	tgc	aga	tct	agt	cag	aac	ctt	gta	cac	agt	aat	gga	aat	acc	tat	624
Ser	Cys	Arg	Ser	Ser	Gln	Asn	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	
		195				200						205				
tta	cat	tgg	tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aat	ctc	ctg	atc	672
Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Asn	Leu	Leu	Ile	
	210					215					220					
tac	aaa	gtt	tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	720
Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	
	225				230					235					240	

agt	gga	tca	ggg	aca	gaa	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	768
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	
				245					250					255		
gag	gat	ctg	gga	gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	ccg	ctc	816
Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	
			260					265					270			
acg	ttc	ggt	gct	ggg	acc	aag	gtg	gag	ctg	aaa	cgg	gcg	gcc	gca	ggt	864
Thr	Phe	Gly	Ala	Gly	Thr	Lys	Val	Glu	Leu	Lys	Arg	Ala	Ala	Ala	Gly	
		275					280					285				
gcg	ccg	gtg	ccg	tat	ccg	gat	ccg	ctg	gaa	ccg	cgt	gcc	gca	tag		909
Ala	Pro	Val	Pro	Tyr	Pro	Asp	Pro	Leu	Glu	Pro	Arg	Ala	Ala			
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	1			5					10					15		
aac	gtg	aaa	aaa	tta	tta	ttc	gca	att	cct	tta	gtt	gtt	cct	ttc	tat	96
Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro	Phe	Tyr	
			20					25					30			
gcg	gcc	cag	ccg	gcc	atg	gcc	cag	gtg	aag	ctg	cag	cag	tct	gga	cct	144
Ala	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Gln	Ser	Gly	Pro	
		35					40					45				
ggc	cta	gtg	cag	ccc	tca	cag	agc	ctg	tcc	ttc	atc	tgc	aca	gtc	tct	192
Gly	Leu	Val	Gln	Pro	Ser	Gln	Ser	Leu	Ser	Phe	Ile	Cys	Thr	Val	Ser	
	50					55					60					
ggt	ttc	tca	tta	act	agt	cat	ggt	gta	cac	tgg	gtt	cgc	cag	tct	cca	240
Gly	Phe	Ser	Leu	Thr	Ser	His	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	
	65				70					75					80	
gga	aag	ggt	ctg	gag	tgg	ctg	gga	gtg	ata	tgg	ggt					

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aca gcc ata tat tac tgt gcc aga aat agg tac gag agc tac ttt gac 432
Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
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tac tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc ggt 480
Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
145 150 155 160

tca ggc gga ggt ggc tct ggc ggt ggc gga tcc gac atc gag ctc act 528
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
165 170 175

cag tct cca ctc tcc ctg cct gtc agt ctt gga gat cag gcc tcc atc 576
Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
180 185 190

tct tgc aga tct agt cag aac ctt gta cac agt aat gga aat acc tat 624
Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr
195 200 205

tta cat tgg tac ctg cag aag cca ggc cag tct cca aat ctc ctg atc 672
Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile
210 215 220

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Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
225 230 235 240

agt gga tca ggg aca gaa ttc aca ctc aag atc agc aga gtg gag gct 768
Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
245 250 255

gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg ctc 816
Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu
260 265 270

acg ttc ggt gct ggg acc aag gtg gag ctg aaa cgg gcg gcc gca ggt 864
Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Gly
275 280 285

gcg ccg gtg ccg tat ccg gat ccg ctg gaa ccg cgt gcc gca aag aag 912
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aag tag 918
Lys
305

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<210> 43

<211> 5

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of heavy chain CDR-1

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<223> Description of Artificial Sequence: Amino acid
sequence of light chain CDR-2
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<400> 47

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
 1 5 10

<210> 48

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
 sequence of light chain CDR-3

<400> 48

Ser Gln Ser Thr His Val Pro Leu Thr
 1 5

<210> 49

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 49

gtcccaggat cctctgaagc agtcaggccc

30

<210> 50

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 50

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30

<210> 51

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 51

tgtgccctcg aggtgactca aactccactc tc

32

<210> 52

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 52

atggatacta gtggtgcagc atcagccc

28

<210> 53

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 53

ctcttgagg aggtgccag

20

<210> 54

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 54

ccagatttca actgctcatc aga

23

<210> 55

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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43

<210> 56

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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27

20250404 14:00:00

<210> 57
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 57
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32

<210> 58
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 58
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25

<210> 59
 <211> 305
 <212> PRT
 <213> Mus sp.

<400> 59
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15
 Ala Gln Pro Ala Met Ala Asp Ile Val Leu Thr Gln Ser Pro Ala Ser
 20 25 30
 Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser
 35 40 45
 Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln
 50 55 60
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu
 65 70 75 80
 Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95
 Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
 100 105 110
 Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr
 115 120 125
 Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
145 150 155 160

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
165 170 175

Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly
180 185 190

Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr
195 200 205

Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
210 215 220

Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala
225 230 235 240

Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp
245 250 255

Gly Arg Gly Thr Leu Val Thr Val Ser Ala Ala Ala Ala Asp Tyr Lys
260 265 270

Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
275 280 285

Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr
290 295 300

Lys
305

<210> 60

<211> 305

<212> PRT

<213> Mus sp.

<400> 60

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu
20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly
50 55 60

Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala
65 70 75 80

Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
85 90 95

Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
 100 105 110
 Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala
 115 120 125
 Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly
 130 135 140
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr
 145 150 155 160
 Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
 165 170 175
 Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met
 180 185 190
 Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 195 200 205
 Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 210 215 220
 Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu
 225 230 235 240
 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr
 245 250 255
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Asp Tyr Lys
 260 265 270
 Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
 275 280 285
 Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr
 290 295 300

Lys
 305

<210> 61
 <211> 118
 <212> PRT
 <213> Mus sp.

<400> 61
 Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp Gly Arg Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ala
 115

<210> 62
 <211> 111
 <212> PRT
 <213> Mus sp.

<400> 62
 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30
 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80
 Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser
 85 90 95
 Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 63
 <211> 117
 <212> PRT
 <213> Mus sp.

<400> 63
 Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1 5 10 15
 Ser Leu Ser Phe Ile Cys Thr Val Ser Gly Phe Ser Leu Thr Ser His
 20 25 30
 Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45

Gly Val Ile Trp Gly Ala Gly Arg Thr Asp Tyr Asn Ala Ala Phe Ile
50 55 60

Ser Arg Leu Ser Ile Ser Arg Asp Ile Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Val Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Asn Arg Tyr Glu Ser Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Ser Leu Thr Val Ser
115

<210> 64

<211> 113

<212> PRT

<213> Mus sp.

<400> 64

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Asn Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys
100 105 110

Arg

<210> 65

<211> 302

<212> PRT

<213> Mus sp.

<400> 65

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
1 5 10 15

Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
20 25 30

Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
 35 40 45
 Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser
 50 55 60
 Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
 65 70 75 80
 Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
 85 90 95
 Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile
 100 105 110
 Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp
 115 120 125
 Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
 130 135 140
 Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 145 150 155 160
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
 165 170 175
 Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
 180 185 190
 Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr
 195 200 205
 Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile
 210 215 220
 Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
 225 230 235 240
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
 245 250 255
 Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu
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 Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Gly
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 Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala
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<210> 66
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Ala	Ala	Gln 35	Pro	Ala	Met	Ala	Gln 40	Val	Lys	Leu	Gln	Gln 45	Ser	Gly	Pro
Gly	Leu 50	Val	Gln	Pro	Ser	Gln 55	Ser	Leu	Ser	Phe	Ile 60	Cys	Thr	Val	Ser
Gly 65	Phe	Ser	Leu	Thr	Ser 70	His	Gly	Val	His	Trp 75	Val	Arg	Gln	Ser	Pro 80
Gly	Lys	Gly	Leu	Glu 85	Trp	Leu	Gly	Val	Ile 90	Trp	Gly	Ala	Gly	Arg 95	Thr
Asp	Tyr	Asn 100	Ala	Ala	Phe	Ile	Ser	Arg 105	Leu	Ser	Ile	Ser	Arg 110	Asp	Ile
Ser	Lys	Ser 115	Gln	Val	Phe	Phe	Lys 120	Met	Asn	Ser	Leu	Gln 125	Val	Asp	Asp
Thr 130	Ala	Ile	Tyr	Tyr	Cys 135	Ala	Arg	Asn	Arg	Tyr	Glu 140	Ser	Tyr	Phe	Asp
Tyr 145	Trp	Gly	Gln	Gly	Thr 150	Thr	Val	Thr	Val	Ser 155	Ser	Gly	Gly	Gly	Gly 160
Ser	Gly	Gly	Gly 165	Gly	Ser	Gly	Gly	Gly	Gly 170	Ser	Asp	Ile	Glu	Leu 175	Thr
Gln	Ser	Pro 180	Leu	Ser	Leu	Pro	Val	Ser 185	Leu	Gly	Asp	Gln	Ala 190	Ser	Ile
Ser	Cys 195	Arg	Ser	Ser	Gln	Asn 200	Leu	Val	His	Ser	Asn 205	Gly	Asn	Thr	Tyr
Leu 210	His	Trp	Tyr	Leu	Gln 215	Lys	Pro	Gly	Gln	Ser	Pro 220	Asn	Leu	Leu	Ile
Tyr 225	Lys	Val	Ser	Asn 230	Arg	Phe	Ser	Gly	Val	Pro 235	Asp	Arg	Phe	Ser	Gly 240
Ser	Gly	Ser	Gly 245	Thr	Glu	Phe	Thr	Leu	Lys 250	Ile	Ser	Arg	Val	Glu 255	Ala
Glu	Asp	Leu 260	Gly	Val	Tyr	Phe	Cys 265	Ser	Gln	Ser	Thr	His 270	Val	Pro	Leu
Thr	Phe 275	Gly	Ala	Gly	Thr	Lys 280	Val	Glu	Leu	Lys	Arg 285	Ala	Ala	Ala	Gly
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Lys
305

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